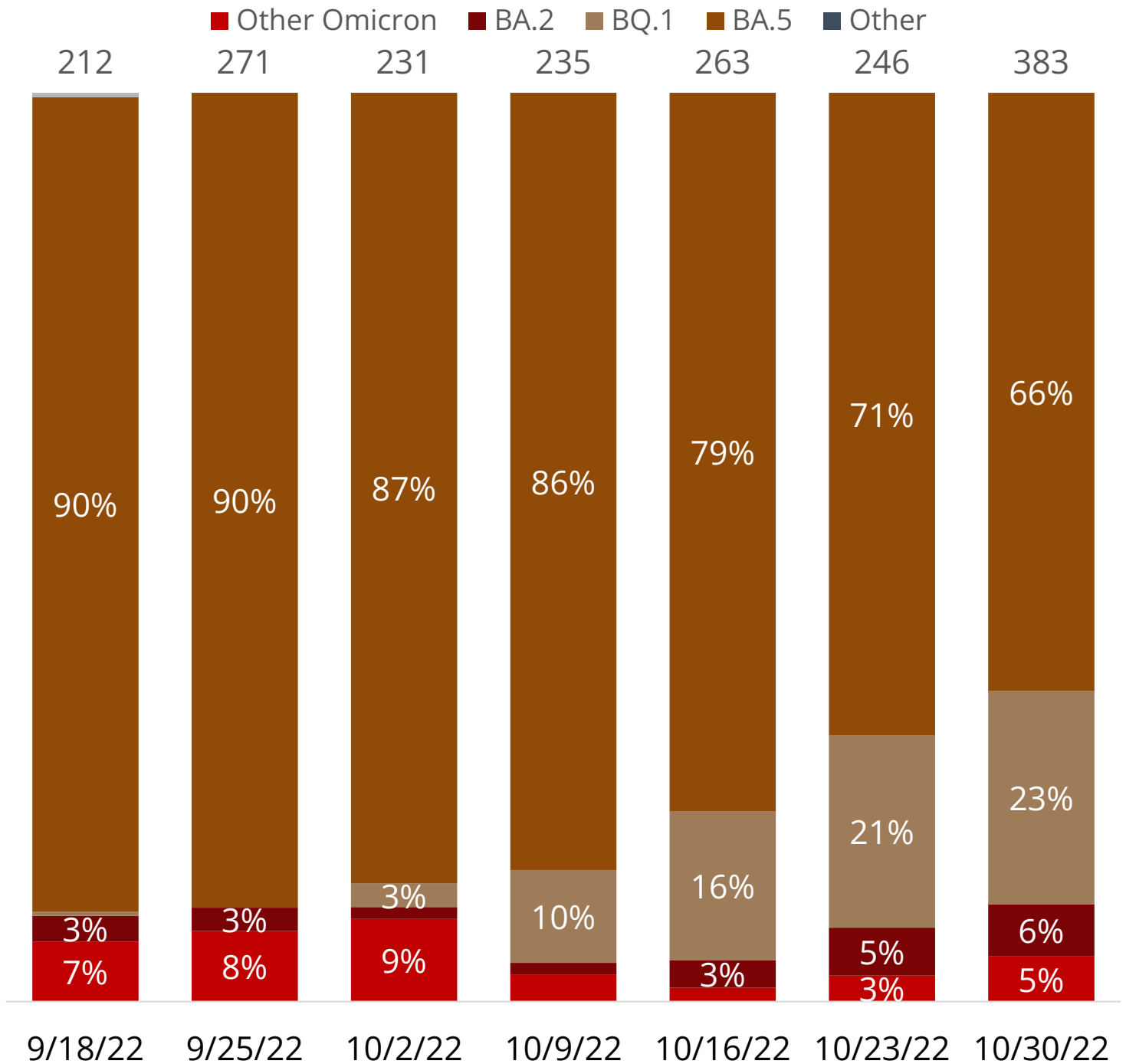




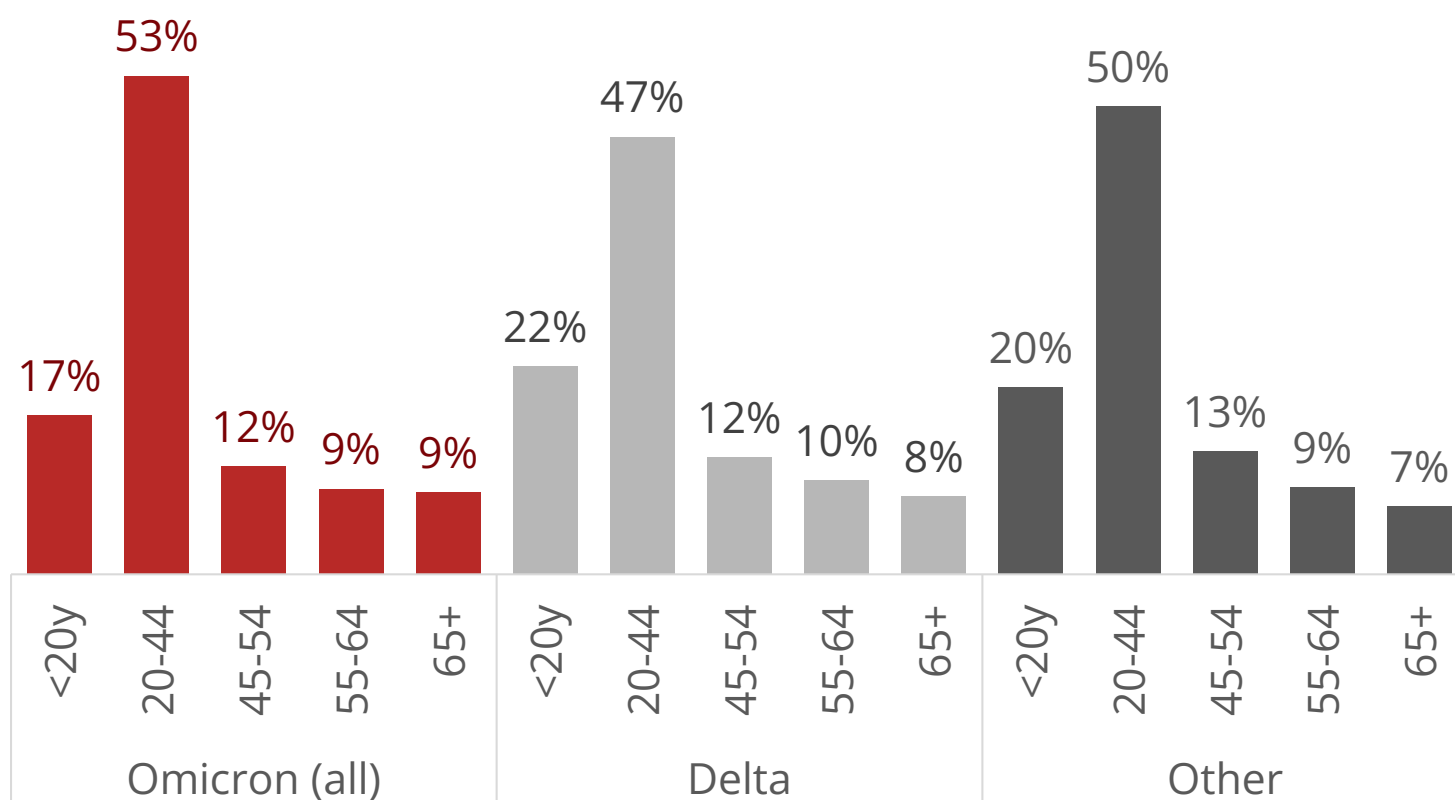
BA.4 and BA.5 became the predominant Omicron sub-variants in June 2022. Proportions of the BA.5 sub-variant BQ.1 grew during October 2022.



Week of specimen collection

Data timeframe represented above: 9/18/2022 to 11/5/2022

Sequenced COVID-19 cases, by variant, for each age group and county



County of Residence	Omicron (other)	Omicron BQ.1	Delta	Other	Total Sequenced
Apache	46.2%	1.0%	38.6%	14.1%	604
Cochise	52.6%	0.5%	34.0%	12.5%	956
Coconino	48.2%	0.1%	31.8%	19.7%	9,388
Gila	17.2%	0.4%	53.2%	29.1%	261
Graham	42.2%	0.4%	34.0%	23.5%	230
Greenlee	19.5%	0.0%	75.6%	4.8%	41
La Paz	46.3%	0.0%	34.1%	19.5%	41
Maricopa	47.7%	0.2%	31.5%	20.1%	61,120
Mohave	29.0%	0.0%	53.3%	17.1%	1,945
Navajo	45.8%	1.2%	38.9%	13.6%	1,320
Pima	41.9%	0.2%	40.4%	16.5%	11,621
Pinal	31.0%	0.1%	45.9%	22.2%	4,139
Santa Cruz	48.9%	0.8%	34.6%	15.7%	485
Yavapai	28.3%	0.0%	56.4%	14.0%	1,382
Yuma	38.9%	0.0%	44.5%	16.3%	1,831
Totals	43,332	214	32,984	18,443	95,364

Data timeframe represented above: 1/1/2021 to 11/5/2022

NOTE: Omicron (other) includes all sub-lineages except for BQ.1

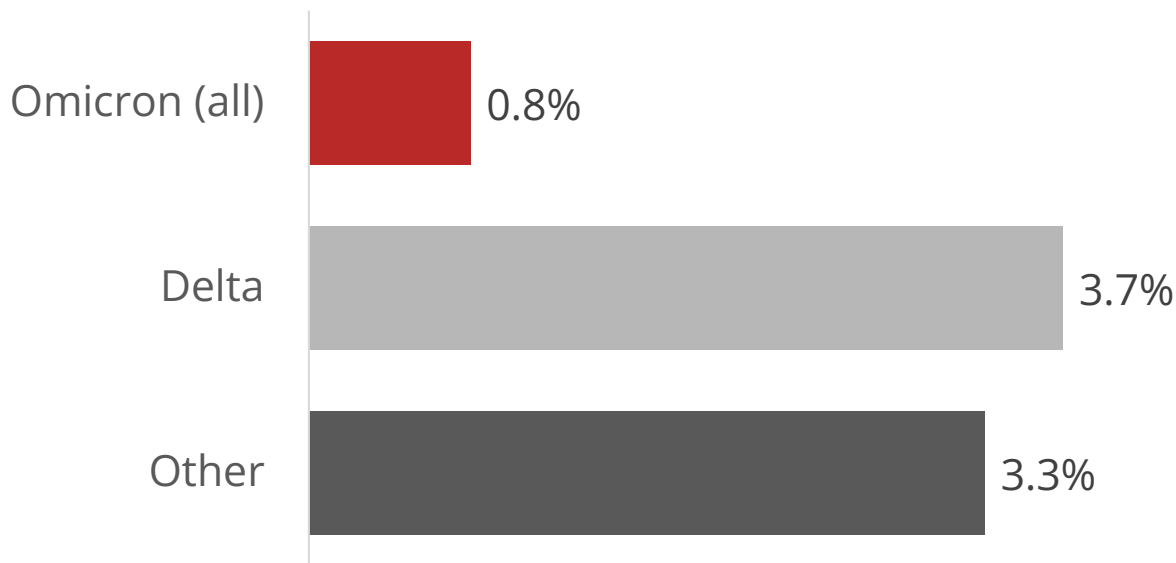
Hospitalizations and deaths of COVID-19 cases, by variant

These graphs show the proportion of sequenced cases for each variant that were hospitalized or died due to COVID-19.

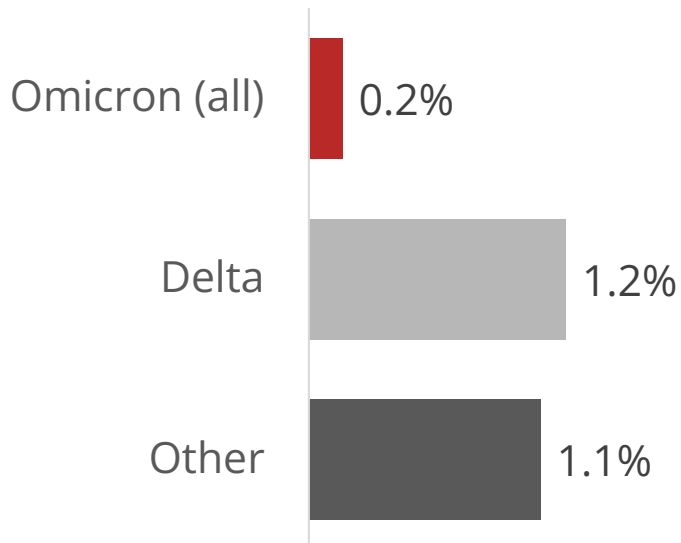
At this time, cases with the Omicron variant were less likely to be hospitalized or die compared to other sequenced cases.

Omicron includes all of its circulating sub-variants in AZ.

Hospitalizations



Deaths

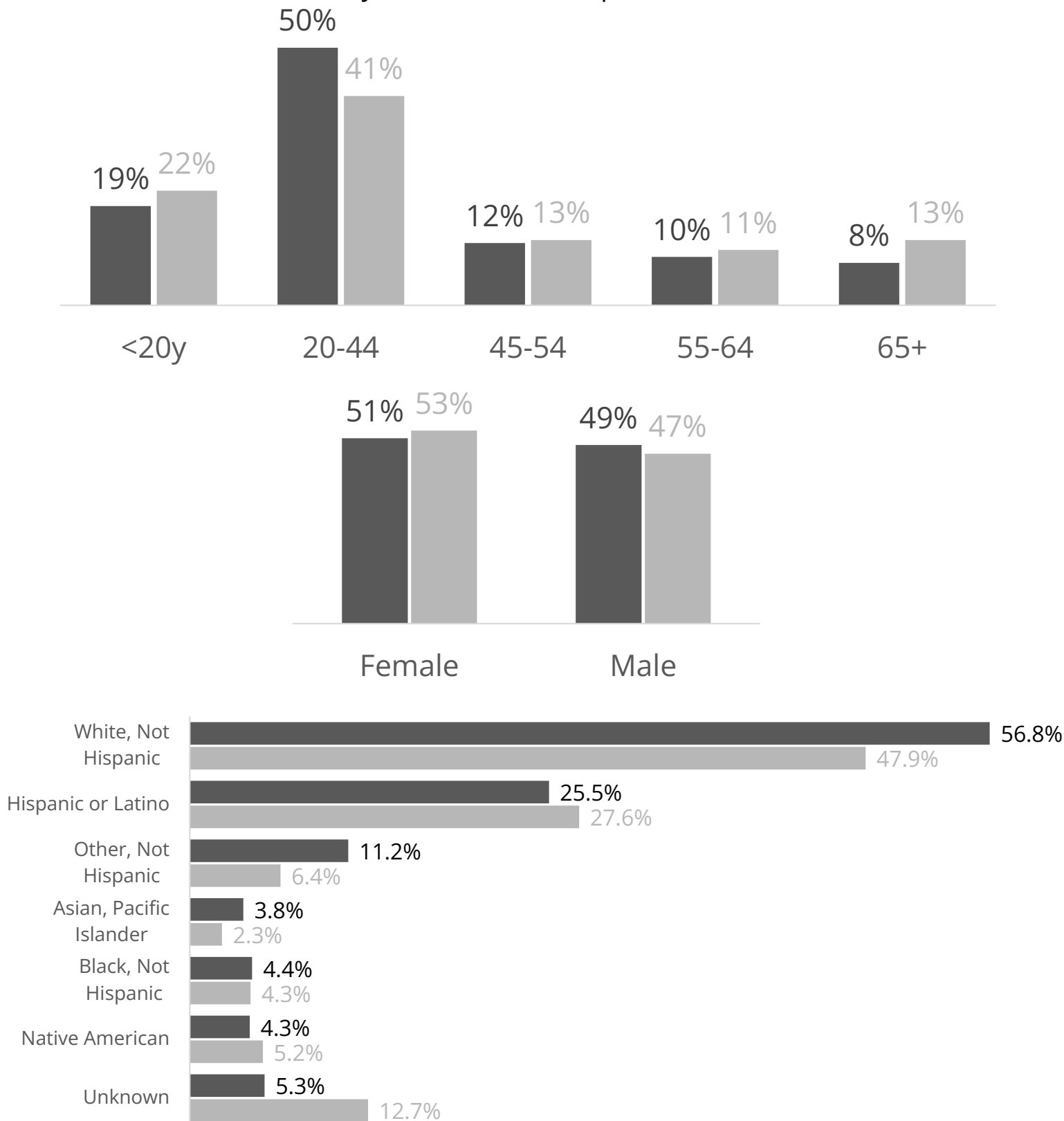


These numbers will change as more information about hospitalizations and deaths is received by ADHS for sequenced cases.

Data timeframe represented above: 1/1/2021 to 11/5/2022

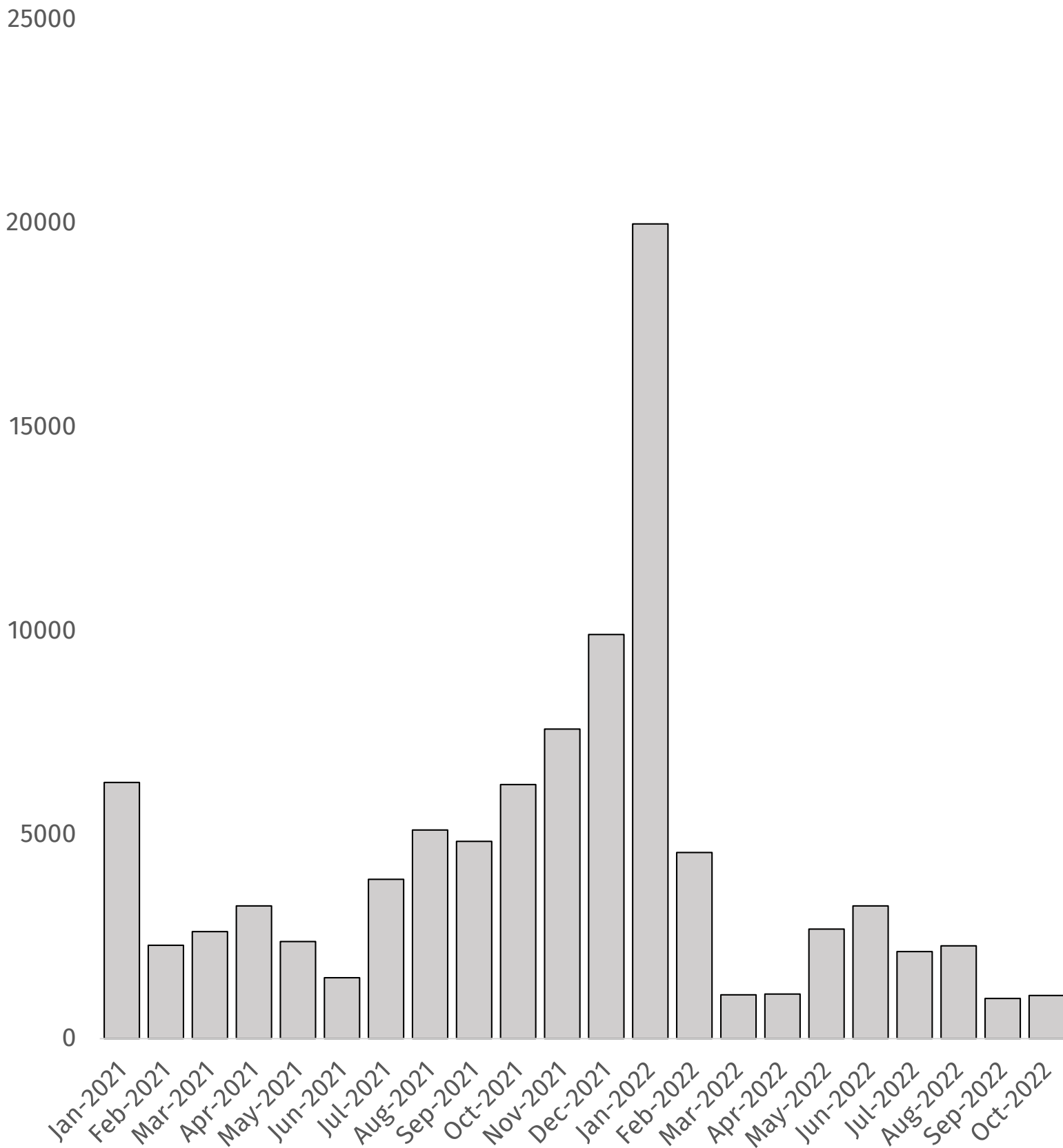
Proportion of COVID-19 cases sequenced compared to case demographics

Demographics for Arizona's sequenced cases resemble those for all 2021 through November 5, 2022 COVID-19 cases, although a higher proportion of cases aged 20-44 years have been sequenced.



Data timeframe represented above: 1/1/2021 to 11/5/2022

Number of COVID-19 cases sequenced, by month of specimen collection



Data timeframe represented above: 1/1/2021 to 10/31/2022

About the data:

- Facilities performing laboratory tests for COVID-19 report positive COVID-19 test results to ADHS pursuant to Arizona Administrative Code R9-6-204.
- Laboratories collect specimens from across the state. Sequencing is performed by specialized laboratories on a sample of specimens. The sequencing results are sent to ADHS and matched to case data.
- The sequencing data shown in this report represent lineage data that has been matched to reported and confirmed COVID-19 cases. Only one sequencing result is shown for a case with multiple results.
- The data time frame on page 1 (cases with sequenced specimens collected within a rolling 7-week period) was selected to better show the prevalence of current circulating variants. The lineages shown will vary to best reflect recent variants of concern circulating in Arizona. In this week's report:
 - BA.2 includes all sub-variants (BA.2.3, BG.2, BN.1, etc.).
 - BA.5 includes all sub-variants respectively (BF.1, BE.1, etc.) except BQ.1.
 - The BA.5 sub-variant BQ.1 is represented separately.
- The remainder of the report includes the total accumulated cases with sequenced specimens collected January 1, 2021 to November 5, 2022.
 - This data was compiled, verified, and matched by ADHS .
- Sequencing data is derived from whole genome sequencing performed on a proportion of positive COVID-19 samples in Arizona. Not every positive sample for COVID-19 is sequenced.
- ADHS receives data from various partners, affecting the timing of when summarized sequencing data will be available for any given period. Samples are collected, tested for COVID-19, delivered to the respective laboratories then sequenced. ADHS partners validate the quality of the data and report the results. There is time between each step of the process for matching sequence data to case data.
- COVID-19 sequencing data is reported to ADHS at a rapid rate. Interpretation of the data presented should consider that sequencing data is continuously updated.
- Please consult with public health if making clinical decisions based on circulating variant proportions.